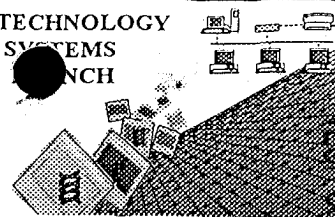


1600
1655

BIOTECHNOLOGY
SYSTEMS
ANCH



TECH CENTER 1600/2900

JAN 16 2001

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CRF Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: 09 635 027

Filing Date: 4 Aug 2000

Date Processed by STIC: Nov 13, 2001

STIC Contact: Mark Spencer, 703-308-4212

Nature of Problem:

The CRF (was):

☐ (circle one) Damaged or Unreadable (for Unreadable, see attached)

☐ Blank (no files on CRF) (see attached)

☐ Empty file (filename present, but no bytes in file) (see attached)

☐ Virus-infected. Virus name: _____ The STIC will not process the CRF.

☐ Not saved in ASCII text

☐ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should **only** be the Sequence Listing.

☒ Did not contain a Sequence Listing. (see attached sample)

☐ Other: _____

**PLEASE USE THE CHECKER VERSION 3.0 PROGRAM TO REDUCE ERRORS.
SEE BELOW FOR DETAILS:**

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

NF-kappa B sequence on step 63 was obtained from HIV-1 (nt 349-374, nt 9434-9458)

K03455. Human immunodeficiency virus type 1 [gi:1906382]

Related Sequences,

Protein, PubMed, Taxonomy

LOCUS HIVHXB2CG 9719 bp ss-RNA VRL 19-AUG-1999
DEFINITION Human immunodeficiency virus type 1 (HXB2), complete genome;
HIV1/HTLV-III/LAV reference genome.
ACCESSION K03455 M38432
VERSION K03455.1 GI:1906382
KEYWORDS TAR protein; acquired immune deficiency syndrome; complete genome;
env protein; gag protein; long terminal repeat (LTR); pol protein;
polyprotein; proviral gene; reverse transcriptase; transactivator.
SOURCE Human immunodeficiency virus type 1.
ORGANISM Human immunodeficiency virus type 1
Viruses; Retroviral viruses; Retroviridae; Lentivirus; Primate
lentivirus group.

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ORGANISM Human immunodeficiency virus type 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
REFERENCE 1 (bases 493 to 674; 9577 to 9718)
AUTHORS Ratner,L., Haseltine,W., Patarca,R., Livak,K.J., Starcich,B.,
Josephs,S.F., Doran,E.R., Rafalski,J.A., Whitehorn,E.A.,
Baumeister,K., Ivanoff,L., Petteway,S.R. Jr., Pearson,M.L.,
Lautenberger,J.A., Papas,T.S., Ghrayeb,J., Chang,N.T., Gallo,R.C.
and Wong-Staal,F.
TITLE Complete nucleotide sequence of the AIDS virus, HTLV-III
JOURNAL Nature 313 (6000), 277-284 (1985)
MEDLINE 85111123
PUBMED 2578615
REFERENCE 2 (bases 1 to 653)
AUTHORS Starcich,B., Ratner,L., Josephs,S.F., Okamoto,T., Gallo,R.C.

*Beginning of file
11/16/01 mtharper*

FEATURES	Location/Qualifiers
source	1..9719 /organism="Human immunodeficiency virus type 1" /proviral /isolate="HXB2" /db_xref="taxon:11676" /note="HTLV-III/LAV"
LTR	1..634 /note="5' LTR"
repeat_region	454..551 /note="R repeat 5' copy"
mRNA	455..9635 /product="HXB2 genomic mRNA"
prim_transcript	455..9635 /note="tat, trs, 27K subgenomic mRNA"
intron	744..5777 /note="tat, trs, 27K mRNA intron 1"
CDS	790..2292 /note="gag polyprotein" /codon_start=1 /protein_id="AAB50258.1" /db_xref="GI:327745"

/translation="MGARASVLSGGELDRWEKIRLRPGGKKKYKLKHIVWASRELERF
AVNPGLLETSEGCRLQILGQLQPSLQTGSEELRSLYNTVATLYCVHQRIEIKDTKEALD
KIEEEQNKSKKKAQQAAADTGHSNQVSQNYPIVQNIQGMVHQALSPRTLNAWVKVVE
EKAFSPEVIPMFSALESGATPQDLNMTLNTVGGHQAAMQMLKETINEEAAEWDRVHPV
HAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMTNNPPIPVGEIYKRWIILGLNKIVRM
YSPTSILDIRQGPKEPFRDYVDRFYKTLRAEQASQEVKNWMTETLLVQANPDCKTIL
KALGPAATLEEMMTACQGVGGPGHKARVLAEAMSQVTNSATIMMQRGNFRNQKIVKC
FNCGKEGHTARNCRAPRKKGCWKCGKEGHQMKDCTERQANFLGKIWPSYKGRPGNFLQ
SRPEPTAPPEESFRSGVETTTTPQKQEPIDKELYPLTSLRSLFGNDPSSQ"

CDS	2358..5096 /note="pol polyprotein (NH2-terminus uncertain)" /codon_start=1
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1. Sample of file contents
This is not an intelligible
sequence listing.
2. Sequence listing as presented is
"embedded" within some other
type of file.

Mr Harper